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Form PTO 1449 U.S. Department of Commerce Patent and Trademark Office	ATTY DOCKET NO: P-TB 5067	SERIAL NO. 10/032,395
	APPLICANT: Hansen et al.	
INFORMATION DISCLOSURE STATEMENT BY APPLICANT	FILING DATE: December 21, 2001	GROUP: 1651

U.S. PATENT DOCUMENTS

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FOREIGN PATENT DOCUMENTS

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EXAM. INITIALS		DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUB- CLASS	TRANSLATION (YES/NO)

OTHER DOCUMENTS (Including Author, Title, Date, Pertinent Pages)

✓		Gerstein, M., "Measurement of the effectiveness of transitive sequence comparison, through a third 'intermediate' sequence," <u>BIOINFORMATICS</u> , 14(8):707-714 (1998).

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	✓	Altschul et al., "Basic Local Alignment Search Tool," <u>J. Mol. Biol.</u> , 215:403-410 (1990).
	✓	Altschul et al., "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs," <u>Nucleic Acids Res.</u> , 25(17):3389-3402 (1997).
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	INFORMATION DISCLOSURE STATEMENT BY APPLICANT	APPLICANT: Hansen et al.	FILING DATE: December 21, 2001	


✓	Attwood et al., "PRINTS and PRINTS-S shed light on protein ancestry," <u>Nucleic Acids Res.</u> , 30(1):239-241 (2002).
✓	Bateman et al., "The Pfam Protein Families Database," <u>Nucleic Acids Res.</u> , 30(1):276-280 (2002).
✓	Bolten et al., "Clustering protein sequences-structure prediction by transitive homology," <u>Bioinformatics</u> , 17(10):935-941 (2001).
✓	Böhm, "The Computer Program LUDI: A New Method for the De Novo Design of Enzyme Inhibitors," <u>J. Comp. Aided Mol. Des.</u> , 6:61-78 (1992).
✓	Carugo and Argos, "NADP-dependent Enzymes. I: Conserved Stereochemistry of Cofactor Binding," <u>Proteins: Struc., Funct., Genet.</u> , 28:10-28 (1997).
✓	Corpet et al., "ProDom and ProDom-CG: tools for protein domain analysis and whole genome comparisons," <u>Nucleic Acids Res.</u> , 28(1):267-269 (2000).
✓	Henikoff et al., "Increased coverage of protein families with the Blocks Database servers," <u>Nucleic Acids Res.</u> , 28(1):228-230 (2000).
✓	Hofmann et al., "The PROSITE database, its status in 1999," <u>Nucleic Acids Res.</u> , 27(1):215-219 (1999).
✓	Jarvis and Patrick, "Clustering Using a Similarity Measure Based on Shared Near Neighbors," <u>IEEE Trans. Comp.</u> , 22(11):1025-1034 (1973).
✓	Manley, "Multivariate Statistical Methods, a Primer," Chapman Hall Chapter 8:100-113 (1994).
✓	Murzin et al., "SCOP: A Structural Classification of Proteins Database for the Investigation of Sequences and Structures," <u>J. Mol. Biol.</u> , 247:536-540 (1995).

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	INFORMATION DISCLOSURE STATEMENT BY APPLICANT	APPLICANT: Hansen et al.	FILING DATE: December 21, 2001

<input checked="" type="checkbox"/>	Needleman and Wunsch, "A General Method Applicable to the Search for Similarities in the Amino Acid Sequence of Two Proteins," <u>J. Mol. Biol.</u> , 48:443-453 (1970).
<input checked="" type="checkbox"/>	Nicholas et al., "Strategies for Searching Sequence Databases," <u>BioTechniques</u> , 28:1174-1191 (2000).
<input checked="" type="checkbox"/>	Pearson and Lipman, "Improved Tools for Biological Sequence Comparison," <u>Proc. Natl. Acad. Sci. USA</u> , 85:2444-2448 (1988).
<input checked="" type="checkbox"/>	Sali and Blundell, "Comparative Protein Modelling by Satisfaction of Spatial Restraints," <u>J. Mol. Biol.</u> , 234:779-815 (1993).
<input checked="" type="checkbox"/>	Schnur, "Design and Diversity Analysis of Large Combinatorial Libraries Using Cell-Based Methods," <u>J. Chem. Inf. Comput. Sci.</u> , 39:36-45 (1999).
<input checked="" type="checkbox"/>	Sellers, "On the Theory and Computation of Evolutionary Distances," <u>J. Appl. Math.</u> , 26(4):787-793 (1974).
<input checked="" type="checkbox"/>	Sellers, "Pattern Recognition in Genetic Sequences," <u>Proc. Natl. Acad. Sci. USA</u> , 76(7):3041 (1979).
<input checked="" type="checkbox"/>	Smith and Waterman, "Identification of Common Molecular Subsequences," <u>J. Mol. Biol.</u> , 147:195-197 (1981).
<input checked="" type="checkbox"/>	Tatusova and Madden, "BLAST 2 SEQUENCES, A New Tool for Comparing Protein and Nucleotide Sequences," <u>FEMS Microbiol. Lett.</u> , 174:247-250 (1999).
<input checked="" type="checkbox"/>	Waterman and Eggert, "A New Algorithm for Best Subsequence Alignments with Application to tRNA-rRNA Comparisons," <u>J. Mol. Biol.</u> , 197:723-728 (1987).
<input checked="" type="checkbox"/>	Worley et al., "BEAUTY-X: enhanced BLAST searches for DNA queries," <u>Bioinformatics</u> , 14(10):890-891 (1998).

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